

## SEQUENCE LISTING

<110> Sprecher, Cindy A.  
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 Gao, Zeren  
 Whitmore, Theodore E.  
 Kuijper, Joseph L.  
 Maurer, Mark F.

<120> CYTOKINE RECEPTOR ZCYTOR17

<130> 00-42

<150> US 60/214,282

<151> 2000-06-26

<150> US 60/214,955

<151> 2000-06-29

<150> US 60/267,963

<151> 2001-08-02

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<170> FastSEQ for Windows Version 3.0

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Met Met	

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Thr	Gln	Tyr	Thr	Val	Lys	Arg	Thr	Tyr	Ala	Phe	Gly	Glu	Lys	His	Asp		
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Phe	Phe	Leu	Pro	Arg	Ile	Thr	Ile	Pro	Asp	Asn	Tyr	Thr	Ile	Glu	Val		
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ggt caa agt tta gta cca gat cat ctg tgt gag gaa gga gcc cca aat 2288  
Gly Gln Ser Leu Val Pro Asp His Leu Cys Glu Glu Gly Ala Pro Asn  
695 700 705

cca tat ttg aaa aat tca gtg aca gcc agg gaa ttt ctt gtg tct gaa 2336  
Pro Tyr Leu Lys Asn Ser Val Thr Ala Arg Glu Phe Leu Val Ser Glu  
710 715 720

aaa ctt cca gag cac acc aag gga gaa gtc taaatgcgac catagcatga 2386  
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Tyr Tyr Arg Lys Asn Leu Thr Cys Thr Trp Ser Pro Gly Lys Glu Thr  
35 40 45  
Ser Tyr Thr Gln Tyr Thr Val Lys Arg Thr Tyr Ala Phe Gly Glu Lys  
50 55 60  
His Asp Asn Cys Thr Thr Asn Ser Ser Thr Ser Glu Asn Arg Ala Ser  
65 70 75 80  
Cys Ser Phe Phe Leu Pro Arg Ile Thr Ile Pro Asp Asn Tyr Thr Ile  
85 90 95  
Glu Val Glu Ala Glu Asn Gly Asp Gly Val Ile Lys Ser His Met Thr  
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Tyr Trp Arg Leu Glu Asn Ile Ala Lys Thr Glu Pro Pro Lys Ile Phe  
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Arg Val Lys Pro Val Leu Gly Ile Lys Arg Met Ile Gln Ile Glu Trp  
130 135 140

0992949.052501

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Pro	Phe	Thr	Glu	Tyr	Val	Ile	Ala 200	Leu	Arg	Cys	Ala	Val	Lys	Glu	Ser 205
Lys	Phe 210	Trp	Ser	Asp	Trp	Ser	Gln 215	Glu	Lys	Met 220	Gly	Met	Thr	Glu	Glu 225
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Ala	Pro	Val	Leu	Glu	Lys	Thr	Leu	Gly 265	Tyr	Asn	Ile	Trp	Tyr	Tyr	Pro 270
Glu	Ser	Asn 275	Thr	Asn	Leu	Thr	Glu 280	Thr	Met	Asn	Thr	Thr 285	Asn	Gln	Gln 290
Leu 290	Glu	Leu	His	Leu	Gly	Gly	Glu 295	Ser	Phe	Trp	Val	Ser	Met	Ile	Ser 300
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Ala	Glu	Asp	Gln	Leu	Val	Val	Lys	Trp 345	Gln	Ser	Ser	Ala	Leu	Asp	Val 350
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Thr 370	Leu	Ser	Trp	Glu	Ser	Val	Ser 375	Gln	Ala	Thr	Asn 380	Trp	Thr	Ile	Gln 385
Gln 385	Asp	Lys	Leu	Lys	Pro	Phe	Trp	Cys	Tyr	Asn 395	Ile	Ser	Val	Tyr	Pro 400
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Lys	Glu	Gly	Val	Pro	Ser	Glu	Gly	Pro	Glu	Thr	Lys	Val	Glu	Asn	Ile 420
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Arg	Lys 450	Gly	Ile	Ile	Cys	Asn	Tyr	Thr	Ile	Phe	Tyr 460	Gln	Ala	Glu	Gly 465
Gly 465	Lys	Gly	Phe	Ser	Lys	Thr	Val	Asn	Ser	Ser 475	Ile	Leu	Gln	Tyr	Gly 480

Leu Glu Ser Leu Lys Arg Lys Thr Ser Tyr Ile Val Gln Val Met Ala  
 485 490 495  
 Ser Thr Ser Ala Gly Gly Thr Asn Gly Thr Ser Ile Asn Phe Lys Thr  
 500 505 510  
 Leu Ser Phe Ser Val Phe Glu Ile Ile Leu Ile Thr Ser Leu Ile Gly  
 515 520 525  
 Gly Gly Leu Leu Ile Leu Ile Ile Leu Thr Val Ala Tyr Gly Leu Lys  
 530 535 540  
 Lys Pro Asn Lys Leu Thr His Leu Cys Trp Pro Thr Val Pro Asn Pro  
 545 550 555 560  
 Ala Glu Ser Ser Ile Ala Thr Trp His Gly Asp Asp Phe Lys Asp Lys  
 565 570 575  
 Leu Asn Leu Lys Glu Ser Asp Asp Ser Val Asn Thr Glu Asp Arg Ile  
 580 585 590  
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 595 600 605  
 Val Val Asn Phe Gly Asn Val Leu Gln Glu Ile Phe Thr Asp Glu Ala  
 610 615 620  
 Arg Thr Gly Gln Glu Asn Asn Leu Gly Gly Glu Lys Asn Gly Tyr Val  
 625 630 635 640  
 Thr Cys Pro Phe Arg Pro Asp Cys Pro Leu Gly Lys Ser Phe Glu Glu  
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 660 665 670  
 Ser Arg Met Pro Glu Gly Thr Arg Pro Glu Ala Lys Glu Gln Leu Leu  
 675 680 685  
 Phe Ser Gly Gln Ser Leu Val Pro Asp His Leu Cys Glu Glu Gly Ala  
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<221> VARIANT

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<212> DNA

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<221> misc\_feature

<222> (1)...(2196)

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ccngaygtng	aywsngarcc	nacnacnytn	wsntgggarw	sngtnwsnca	rgcnacnaay	1140
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&lt;213&gt; Artificial Sequence

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&lt;223&gt; Oligonucleotide primer ZC12701

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&lt;211&gt; 23

&lt;212&gt; DNA

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T09290" 64626860

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09892949-062601

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T09290-6466860

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gca ctg tgg atg ctc ccc tca ctc tgc aaa ttc agc ctg gca gct ctg 224  
 Ala Leu Trp Met Leu Pro Ser Leu Cys Lys Phe Ser Leu Ala Ala Leu  
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cca gct aag cct gag aac att tcc tgt gtc tac tac tat agg aaa aat 272  
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 25 30 35

tta acc tgc act tgg agt cca gga aag gaa acc agt tat acc cag tac 320  
 Leu Thr Cys Thr Trp Ser Pro Gly Lys Glu Thr Ser Tyr Thr Gln Tyr  
 40 45 50

aca gtt aag aga act tac gct ttt gga gaa aaa cat gat aat tgt aca 368  
 Thr Val Lys Arg Thr Tyr Ala Phe Gly Glu Lys His Asp Asn Cys Thr  
 55 60 65

acc aat agt tct aca agt gaa aat cgt gct tcg tgc tct ttt ttc ctt 416

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Trp	Ser	Gln	Glu	Lys	Met	Gly	Met	Thr	Glu	Glu	Glu	Ala	Pro	Cys	Gly	
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aaa aca ctt ggc tac aac ata tgg tac tat cca gaa agc aac act aac 992  
 Lys Thr Leu Gly Tyr Asn Ile Trp Tyr Tyr Pro Glu Ser Asn Thr Asn  
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ctc aca gaa aca atg aac act act aac cag cag ctt gaa ctg cat ctg 1040  
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 Ser Tyr Thr Gln Tyr Thr Val Lys Arg Thr Tyr Ala Phe Gly Glu Lys  
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 His Asp Asn Cys Thr Thr Asn Ser Ser Thr Ser Glu Asn Arg Ala Ser  
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09892949.062601



Glu Val Glu Ala Glu Asn Gly Asp Gly Val Ile Lys Ser His Met Thr  
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 Tyr Trp Arg Leu Glu Asn Ile Ala Lys Thr Glu Pro Pro Lys Ile Phe  
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 Pro Phe Thr Glu Tyr Val Ile Ala Leu Arg Cys Ala Val Lys Glu Ser  
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&lt;211&gt; 23

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 25 30 35  
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 65          70          75          80
Cys Ser Phe Phe Leu Pro Arg Ile Thr Ile Pro Asp Asn Tyr Thr Ile
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Glu Val Glu Ala Glu Asn Gly Asp Gly Val Ile Lys Ser His Met Thr
100          105          110
Tyr Trp Arg Leu Glu Asn Ile Ala Lys Thr Glu Pro Pro Lys Ile Phe
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165          170          175
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09892949-062601

&lt;220&gt;

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33

&lt;210&gt; 31

&lt;211&gt; 30

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Oligonucleotide primer ZC17313

&lt;400&gt; 31

caccctgcga agccttagca gcagtaggcc

30

&lt;210&gt; 32

&lt;211&gt; 30

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Oligonucleotide primer ZC17205

&lt;400&gt; 32

cccgcccat ccccgtaggac caccttggtg

30

&lt;210&gt; 33

&lt;211&gt; 30

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Oligonucleotide primer ZC17206

&lt;400&gt; 33

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&lt;210&gt; 34

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&lt;212&gt; PRT

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<213> Artificial Sequence

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1 5

<210> 35

<211> 8

<212> PRT

<213> Artificial Sequence

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<223> FLAG tag peptide sequence

<400> 35

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1 5

<210> 36

<211> 699

<212> DNA

<213> Homo sapiens

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acccttgagg	tcacatgcgt	ggtggtggac	gtgagccacg	aagaccctga	ggtcaagttc	180
aactggtacg	tggacggcgt	ggaggtgcat	aatgccaaga	caaagccgcg	ggaggagcag	240
tacaacagca	cgtaccgtgt	ggtcagcgtc	ctcaccgtcc	tgcaccagga	ctggctgaat	300
ggcaaggagt	acaagtgcaa	ggtctccaac	aaagccctcc	catcctccat	cgagaaaacc	360
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gatgagctga	ccaagaacca	ggtcagcctg	acctgcctgg	tcaaaggctt	ctatcccagc	480
gacatcgccg	tggagtggga	gagcaatggg	cagccggaga	acaactacaa	gaccacgcct	540
cccgtgctgg	actccgacgg	ctccttcttc	ctctacagca	agctcaccgt	ggacaagagc	600
aggtggcagc	aggggaacgt	cttctcatgc	tccgtgatgc	atgaggctct	gcacaaccac	660
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<210> 37

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<212> DNA

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&lt;222&gt; (1)...(990)

&lt;400&gt; 37

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Ala	Ser	Thr	Lys	Gly	Pro	Ser	Val	Phe	Pro	Leu	Ala	Pro	Ser	Ser	Lys	
1				5				10					15			

agc	acc	tct	ggg	ggc	aca	gcg	gcc	ctg	ggc	tgc	ctg	gtc	aag	gac	tac	96
Ser	Thr	Ser	Gly	Gly	Thr	Ala	Ala	Leu	Gly	Cys	Leu	Val	Lys	Asp	Tyr	
			20					25					30			

ttc	ccc	gaa	ccg	gtg	acg	gtg	tcg	tgg	aac	tca	ggc	gcc	ctg	acc	agc	144
Phe	Pro	Glu	Pro	Val	Thr	Val	Ser	Trp	Asn	Ser	Gly	Ala	Leu	Thr	Ser	
		35					40					45				

ggc	gtg	cac	acc	ttc	ccg	gct	gtc	cta	cag	tcc	tca	gga	ctc	tac	tcc	192
Gly	Val	His	Thr	Phe	Pro	Ala	Val	Leu	Gln	Ser	Ser	Gly	Leu	Tyr	Ser	
	50					55					60					

ctc	agc	agc	gtg	gtg	acc	gtg	ccc	tcc	agc	agc	ttg	ggc	acc	cag	acc	240
Leu	Ser	Ser	Val	Val	Thr	Val	Pro	Ser	Ser	Ser	Leu	Gly	Thr	Gln	Thr	
65					70				75					80		

tac	atc	tgc	aac	gtg	aat	cac	aag	ccc	agc	aac	acc	aag	gtg	gac	aag	288
Tyr	Ile	Cys	Asn	Val	Asn	His	Lys	Pro	Ser	Asn	Thr	Lys	Val	Asp	Lys	
			85					90						95		

aaa	gtt	gag	ccc	aaa	tct	tgt	gac	aaa	act	cac	aca	tgc	cca	ccg	tgc	336
Lys	Val	Glu	Pro	Lys	Ser	Cys	Asp	Lys	Thr	His	Thr	Cys	Pro	Pro	Cys	
			100					105					110			

cca	gca	cct	gaa	ctc	ctg	ggg	gga	ccg	tca	gtc	ttc	ctc	ttc	ccc	cca	384
Pro	Ala	Pro	Glu	Leu	Leu	Gly	Gly	Pro	Ser	Val	Phe	Leu	Phe	Pro	Pro	
		115				120						125				

aaa	ccc	aag	gac	acc	ctc	atg	atc	tcc	cgg	acc	cct	gag	gtc	aca	tgc	432
Lys	Pro	Lys	Asp	Thr	Leu	Met	Ile	Ser	Arg	Thr	Pro	Glu	Val	Thr	Cys	
	130					135					140					

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gtg gtg gtg gac gtg agc cac gaa gac cct gag gtc aag ttc aac tgg	480
Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp	
145 150 155 160	
tac gtg gac ggc gtg gag gtg cat aat gcc aag aca aag ccg cgg gag	528
Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu	
165 170 175	
gag cag tac aac agc acg tac cgt gtg gtc agc gtc ctc acc gtc ctg	576
Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu	
180 185 190	
cac cag gac tgg ctg aat ggc aag gag tac aag tgc aag gtc tcc aac	624
His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn	
195 200 205	
aaa gcc ctc cca gcc ccc atc gag aaa acc atc tcc aaa gcc aaa ggg	672
Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly	
210 215 220	
cag ccc cga gaa cca cag gtg tac acc ctg ccc cca tcc cgg gat gag	720
Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu	
225 230 235 240	
ctg acc aag aac cag gtc agc ctg acc tgc ctg gtc aaa ggc ttc tat	768
Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr	
245 250 255	
ccc agc gac atc gcc gtg gag tgg gag agc aat ggg cag ccg gag aac	816
Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn	
260 265 270	
aac tac aag acc acg cct ccc gtg ctg gac tcc gac ggc tcc ttc ttc	864
Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe	
275 280 285	
ctc tac agc aag ctc acc gtg gac aag agc agg tgg cag cag ggg aac	912
Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn	
290 295 300	
gtc ttc tca tgc tcc gtg atg cat gag gct ctg cac aac cac tac acg	960
Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr	
305 310 315 320	

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 Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys  
                   325                  330

990

<210> 38  
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 <212> PRT  
 <213> Homo sapiens

<400> 38

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			20				25						30		
Phe	Pro	Glu	Pro	Val	Thr	Val	Ser	Trp	Asn	Ser	Gly	Ala	Leu	Thr	Ser
		35				40						45			
Gly	Val	His	Thr	Phe	Pro	Ala	Val	Leu	Gln	Ser	Ser	Gly	Leu	Tyr	Ser
	50					55					60				
Leu	Ser	Ser	Val	Val	Thr	Val	Pro	Ser	Ser	Ser	Leu	Gly	Thr	Gln	Thr
65					70					75				80	
Tyr	Ile	Cys	Asn	Val	Asn	His	Lys	Pro	Ser	Asn	Thr	Lys	Val	Asp	Lys
			85							90				95	
Lys	Val	Glu	Pro	Lys	Ser	Cys	Asp	Lys	Thr	His	Thr	Cys	Pro	Pro	Cys
			100					105					110		
Pro	Ala	Pro	Glu	Leu	Leu	Gly	Gly	Pro	Ser	Val	Phe	Leu	Phe	Pro	Pro
			115				120					125			
Lys	Pro	Lys	Asp	Thr	Leu	Met	Ile	Ser	Arg	Thr	Pro	Glu	Val	Thr	Cys
	130					135					140				
Val	Val	Val	Asp	Val	Ser	His	Glu	Asp	Pro	Glu	Val	Lys	Phe	Asn	Trp
145					150					155				160	
Tyr	Val	Asp	Gly	Val	Glu	Val	His	Asn	Ala	Lys	Thr	Lys	Pro	Arg	Glu
			165					170						175	
Glu	Gln	Tyr	Asn	Ser	Thr	Tyr	Arg	Val	Val	Ser	Val	Leu	Thr	Val	Leu
			180					185					190		
His	Gln	Asp	Trp	Leu	Asn	Gly	Lys	Glu	Tyr	Lys	Cys	Lys	Val	Ser	Asn
		195				200						205			
Lys	Ala	Leu	Pro	Ala	Pro	Ile	Glu	Lys	Thr	Ile	Ser	Lys	Ala	Lys	Gly
	210					215					220				
Gln	Pro	Arg	Glu	Pro	Gln	Val	Tyr	Thr	Leu	Pro	Pro	Ser	Arg	Asp	Glu
225					230					235				240	
Leu	Thr	Lys	Asn	Gln	Val	Ser	Leu	Thr	Cys	Leu	Val	Lys	Gly	Phe	Tyr
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Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn  
 260 265 270  
 Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe  
 275 280 285  
 Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn  
 290 295 300  
 Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr  
 305 310 315 320  
 Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys  
 325 330

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 <212> DNA  
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 1 5 10 15

ttg aaa tct ggt acc gcc tct gtt gtg tgc ctg ctg aat aac ttc tat 96  
 Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr  
 20 25 30

ccc aga gag gcc aaa gta cag tgg aag gtg gat aac gcc ctc caa tcg 144  
 Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser  
 35 40 45

ggt aac tcc cag gag agt gtc aca gag cag gac agc aag gac agc acc 192  
 Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr  
 50 55 60

tac agc ctc agc agc acc ctg acg ctg agc aaa gca gac tac gag aaa 240  
 Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys  
 65 70 75 80

cac aaa gtc tac gcc tgc gaa gtc acc cat cag ggc ctg agc tcg ccc 288

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His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro  
                     85                    90                    95

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 Val Thr Lys Ser Phe Asn Arg Gly Glu Cys \*  
                     100                    105

321

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                     20                    25                    30  
 Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser  
                     35                    40                    45  
 Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr  
                     50                    55                    60  
 Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys  
 65                    70                    75                    80  
 His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro  
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8

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8

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<212> DNA

<213> Homo sapiens

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aaaacattct ctctccccag ccttcatgtg ttaacctggg g atg atg tgg acc tgg	176
Met Met Trp Thr Trp	
1 5	
gca ctg tgg atg ctc ccc tca ctc tgc aaa ttc agc ctg gca gct ctg	224
Ala Leu Trp Met Leu Pro Ser Leu Cys Lys Phe Ser Leu Ala Ala Leu	
10 15 20	
cca gct aag cct gag aac att tcc tgt gtc tac tac tat agg aaa aat	272
Pro Ala Lys Pro Glu Asn Ile Ser Cys Val Tyr Tyr Tyr Arg Lys Asn	
25 30 35	
tta acc tgc act tgg agt cca gga aag gaa acc agt tat acc cag tac	320
Leu Thr Cys Thr Trp Ser Pro Gly Lys Glu Thr Ser Tyr Thr Gln Tyr	
40 45 50	
aca gtt aag aga act tac gct ttt gga gaa aaa cat gat aat tgt aca	368
Thr Val Lys Arg Thr Tyr Ala Phe Gly Glu Lys His Asp Asn Cys Thr	
55 60 65	
acc aat agt tct aca agt gaa aat cgt gct tcg tgc tct ttt ttc ctt	416
Thr Asn Ser Ser Thr Ser Glu Asn Arg Ala Ser Cys Ser Phe Phe Leu	
70 75 80 85	
cca aga ata acg atc cca gat aat tat acc att gag gtg gaa gct gaa	464
Pro Arg Ile Thr Ile Pro Asp Asn Tyr Thr Ile Glu Val Glu Ala Glu	
90 95 100	
aat gga gat ggt gta att aaa tct cat atg aca tac tgg aga tta gag	512
Asn Gly Asp Gly Val Ile Lys Ser His Met Thr Tyr Trp Arg Leu Glu	
105 110 115	
aac ata gcg aaa act gaa cca cct aag att ttc cgt gtg aaa cca gtt	560
Asn Ile Ala Lys Thr Glu Pro Pro Lys Ile Phe Arg Val Lys Pro Val	
120 125 130	
ttg ggc atc aaa cga atg att caa att gaa tgg ata aag cct gag ttg	608
Leu Gly Ile Lys Arg Met Ile Gln Ile Glu Trp Ile Lys Pro Glu Leu	
135 140 145	
gcg cct gtt tca tct gat tta aaa tac aca ctt cga ttc agg aca gtc	656

Ala	Pro	Val	Ser	Ser	Asp	Leu	Lys	Tyr	Thr	Leu	Arg	Phe	Arg	Thr	Val		
150					155					160					165		
aac	agt	acc	agc	tgg	atg	gaa	gtc	aac	ttc	gct	aag	aac	cgt	aag	gat	704	
Asn	Ser	Thr	Ser	Trp	Met	Glu	Val	Asn	Phe	Ala	Lys	Asn	Arg	Lys	Asp		
				170				175					180				
aaa	aac	caa	acg	tac	aac	ctc	acg	ggg	ctg	cag	cct	ttt	aca	gaa	tat	752	
Lys	Asn	Gln	Thr	Tyr	Asn	Leu	Thr	Gly	Leu	Gln	Pro	Phe	Thr	Glu	Tyr		
			185					190					195				
gtc	ata	gct	ctg	cga	tgt	gcg	gtc	aag	gag	tca	aag	ttc	tgg	agt	gac	800	
Val	Ile	Ala	Leu	Arg	Cys	Ala	Val	Lys	Glu	Ser	Lys	Phe	Trp	Ser	Asp		
		200					205					210					
tgg	agc	caa	gaa	aaa	atg	gga	atg	act	gag	gaa	gaa	gct	cca	tgt	ggc	848	
Trp	Ser	Gln	Glu	Lys	Met	Gly	Met	Thr	Glu	Glu	Glu	Ala	Pro	Cys	Gly		
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ctg	gaa	ctg	tgg	aga	gtc	ctg	aaa	cca	gct	gag	gcg	gat	gga	aga	agg	896	
Leu	Glu	Leu	Trp	Arg	Val	Leu	Lys	Pro	Ala	Glu	Ala	Asp	Gly	Arg	Arg		
230					235				240				245				
cca	gtg	cgg	ttg	tta	tgg	aag	aag	gca	aga	gga	gcc	cca	gtc	cta	gag	944	
Pro	Val	Arg	Leu	Leu	Trp	Lys	Lys	Ala	Arg	Gly	Ala	Pro	Val	Leu	Glu		
			250					255					260				
aaa	aca	ctt	ggc	tac	aac	ata	tgg	tac	tat	cca	gaa	agc	aac	act	aac	992	
Lys	Thr	Leu	Gly	Tyr	Asn	Ile	Trp	Tyr	Tyr	Pro	Glu	Ser	Asn	Thr	Asn		
		265					270					275					
ctc	aca	gaa	aca	atg	aac	act	act	aac	cag	cag	ctt	gaa	ctg	cat	ctg	1040	
Leu	Thr	Glu	Thr	Met	Asn	Thr	Thr	Asn	Gln	Gln	Leu	Glu	Leu	His	Leu		
		280					285					290					
gga	ggc	gag	agc	ttt	tgg	gtg	tct	atg	att	tct	tat	aat	tct	ctt	ggg	1088	
Gly	Gly	Glu	Ser	Phe	Trp	Val	Ser	Met	Ile	Ser	Tyr	Asn	Ser	Leu	Gly		
	295					300					305						
aag	tct	cca	gtg	gcc	acc	ctg	agg	att	cca	gct	att	caa	gaa	aaa	tca	1136	
Lys	Ser	Pro	Val	Ala	Thr	Leu	Arg	Ile	Pro	Ala	Ile	Gln	Glu	Lys	Ser		
310					315				320						325		

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ttt cag tgc att gag gtc atg cag gcc tgc gtt gct gag gac cag cta	1184
Phe Gln Cys Ile Glu Val Met Gln Ala Cys Val Ala Glu Asp Gln Leu	
330 335 340	
gtg gtg aag tgg caa agc tct gct cta gac gtg aac act tgg atg att	1232
Val Val Lys Trp Gln Ser Ser Ala Leu Asp Val Asn Thr Trp Met Ile	
345 350 355	
gaa tgg ttt ccg gat gtg gac tca gag ccc acc acc ctt tcc tgg gaa	1280
Glu Trp Phe Pro Asp Val Asp Ser Glu Pro Thr Thr Leu Ser Trp Glu	
360 365 370	
tct gtg tct cag gcc acg aac tgg acg atc cag caa gat aaa tta aaa	1328
Ser Val Ser Gln Ala Thr Asn Trp Thr Ile Gln Gln Asp Lys Leu Lys	
375 380 385	
cct ttc tgg tgc tat aac atc tct gtg tat cca atg ttg cat gac aaa	1376
Pro Phe Trp Cys Tyr Asn Ile Ser Val Tyr Pro Met Leu His Asp Lys	
390 395 400 405	
gtt ggc gag cca tat tcc atc cag gct tat gcc aaa gaa ggc gtt cca	1424
Val Gly Glu Pro Tyr Ser Ile Gln Ala Tyr Ala Lys Glu Gly Val Pro	
410 415 420	
tca gaa ggt cct gag acc aag gtg gag aac att ggc gtg aag acg gtc	1472
Ser Glu Gly Pro Glu Thr Lys Val Glu Asn Ile Gly Val Lys Thr Val	
425 430 435	
acg atc aca tgg aaa gag att ccc aag agt gag aga aag ggt atc atc	1520
Thr Ile Thr Trp Lys Glu Ile Pro Lys Ser Glu Arg Lys Gly Ile Ile	
440 445 450	
tgc aac tac acc atc ttt tac caa gct gaa ggt gga aaa gga ttc tcc	1568
Cys Asn Tyr Thr Ile Phe Tyr Gln Ala Glu Gly Gly Lys Gly Phe Ser	
455 460 465	
aag aca gtc aat tcc agc atc ttg cag tac ggc ctg gag tcc ctg aaa	1616
Lys Thr Val Asn Ser Ser Ile Leu Gln Tyr Gly Leu Glu Ser Leu Lys	
470 475 480 485	
cga aag acc tct tac att gtt cag gtc atg gcc agc acc agt gct ggg	1664

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Arg	Lys	Thr	Ser	Tyr	Ile	Val	Gln	Val	Met	Ala	Ser	Thr	Ser	Ala	Gly	
				490					495					500		
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Gly	Thr	Asn	Gly	Thr	Ser	Ile	Asn	Phe	Lys	Thr	Leu	Ser	Phe	Ser	Val	
			505					510					515			
ttt	gag	att	atc	ctc	ata	act	tct	ctg	att	ggg	gga	ggc	ctt	ctt	att	1760
Phe	Glu	Ile	Ile	Leu	Ile	Thr	Ser	Leu	Ile	Gly	Gly	Gly	Leu	Leu	Ile	
			520					525					530			
ctc	att	atc	ctg	aca	gtg	gca	tat	ggg	ctc	aaa	aaa	ccc	aac	aaa	ttg	1808
Leu	Ile	Ile	Leu	Thr	Val	Ala	Tyr	Gly	Leu	Lys	Lys	Pro	Asn	Lys	Leu	
			535					540				545				
act	cat	ctg	tgt	tgg	ccc	acc	gtt	ccc	aac	cct	gct	gaa	agt	agt	ata	1856
Thr	His	Leu	Cys	Trp	Pro	Thr	Val	Pro	Asn	Pro	Ala	Glu	Ser	Ser	Ile	
550					555					560					565	
gcc	aca	tgg	cat	gga	gat	gat	ttc	aag	gat	aag	cta	aac	ctg	aag	gag	1904
Ala	Thr	Trp	His	Gly	Asp	Asp	Phe	Lys	Asp	Lys	Leu	Asn	Leu	Lys	Glu	
				570					575					580		
tct	gat	gac	tct	gtg	aac	aca	gaa	gac	agg	atc	tta	aaa	cca	tgt	tcc	1952
Ser	Asp	Asp	Ser	Val	Asn	Thr	Glu	Asp	Arg	Ile	Leu	Lys	Pro	Cys	Ser	
			585					590					595			
acc	ccc	agt	gac	aag	ttg	gtg	att	gac	aag	ttg	gtg	gtg	aac	ttt	ggg	2000
Thr	Pro	Ser	Asp	Lys	Leu	Val	Ile	Asp	Lys	Leu	Val	Val	Asn	Phe	Gly	
			600					605				610				
aat	gtt	ctg	caa	gaa	att	ttc	aca	gat	gaa	gcc	aga	acg	ggg	cag	gaa	2048
Asn	Val	Leu	Gln	Glu	Ile	Phe	Thr	Asp	Glu	Ala	Arg	Thr	Gly	Gln	Glu	
			615					620				625				
aac	aat	tta	gga	ggg	gaa	aag	aat	ggg	act	aga	att	ctg	tct	tcc	tgc	2096
Asn	Asn	Leu	Gly	Gly	Glu	Lys	Asn	Gly	Thr	Arg	Ile	Leu	Ser	Ser	Cys	
630					635				640						645	
cca	act	tca	ata	taagtgtgga	ctaaaatg	cg	agaaagg	tgt	cctgtggtct							2148
Pro	Thr	Ser	Ile													

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atgcaaatta gaaaggacat gcagagtttt ccaactagga agactgaatc tgtggcccca 2208  
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<210> 46

<211> 649

<212> PRT

<213> Homo sapiens

<400> 46

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			20					25					30		
Tyr	Tyr	Arg	Lys	Asn	Leu	Thr	Cys	Thr	Trp	Ser	Pro	Gly	Lys	Glu	Thr
		35					40					45			
Ser	Tyr	Thr	Gln	Tyr	Thr	Val	Lys	Arg	Thr	Tyr	Ala	Phe	Gly	Glu	Lys
		50				55					60				
His	Asp	Asn	Cys	Thr	Thr	Asn	Ser	Ser	Thr	Ser	Glu	Asn	Arg	Ala	Ser
65					70					75					80
Cys	Ser	Phe	Phe	Leu	Pro	Arg	Ile	Thr	Ile	Pro	Asp	Asn	Tyr	Thr	Ile
				85					90					95	
Glu	Val	Glu	Ala	Glu	Asn	Gly	Asp	Gly	Val	Ile	Lys	Ser	His	Met	Thr
			100					105					110		
Tyr	Trp	Arg	Leu	Glu	Asn	Ile	Ala	Lys	Thr	Glu	Pro	Pro	Lys	Ile	Phe
		115					120					125			
Arg	Val	Lys	Pro	Val	Leu	Gly	Ile	Lys	Arg	Met	Ile	Gln	Ile	Glu	Trp
		130				135					140				
Ile	Lys	Pro	Glu	Leu	Ala	Pro	Val	Ser	Ser	Asp	Leu	Lys	Tyr	Thr	Leu
145					150					155					160
Arg	Phe	Arg	Thr	Val	Asn	Ser	Thr	Ser	Trp	Met	Glu	Val	Asn	Phe	Ala
				165					170					175	
Lys	Asn	Arg	Lys	Asp	Lys	Asn	Gln	Thr	Tyr	Asn	Leu	Thr	Gly	Leu	Gln
			180					185					190		
Pro	Phe	Thr	Glu	Tyr	Val	Ile	Ala	Leu	Arg	Cys	Ala	Val	Lys	Glu	Ser
		195					200					205			
Lys	Phe	Trp	Ser	Asp	Trp	Ser	Gln	Glu	Lys	Met	Gly	Met	Thr	Glu	Glu
210						215					220				

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Glu Ala Pro Cys Gly Leu Glu Leu Trp Arg Val Leu Lys Pro Ala Glu  
 225 230 235 240  
 Ala Asp Gly Arg Arg Pro Val Arg Leu Leu Trp Lys Lys Ala Arg Gly  
 245 250 255  
 Ala Pro Val Leu Glu Lys Thr Leu Gly Tyr Asn Ile Trp Tyr Tyr Pro  
 260 265 270  
 Glu Ser Asn Thr Asn Leu Thr Glu Thr Met Asn Thr Thr Asn Gln Gln  
 275 280 285  
 Leu Glu Leu His Leu Gly Gly Glu Ser Phe Trp Val Ser Met Ile Ser  
 290 295 300  
 Tyr Asn Ser Leu Gly Lys Ser Pro Val Ala Thr Leu Arg Ile Pro Ala  
 305 310 315 320  
 Ile Gln Glu Lys Ser Phe Gln Cys Ile Glu Val Met Gln Ala Cys Val  
 325 330 335  
 Ala Glu Asp Gln Leu Val Val Lys Trp Gln Ser Ser Ala Leu Asp Val  
 340 345 350  
 Asn Thr Trp Met Ile Glu Trp Phe Pro Asp Val Asp Ser Glu Pro Thr  
 355 360 365  
 Thr Leu Ser Trp Glu Ser Val Ser Gln Ala Thr Asn Trp Thr Ile Gln  
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 Gln Asp Lys Leu Lys Pro Phe Trp Cys Tyr Asn Ile Ser Val Tyr Pro  
 385 390 395 400  
 Met Leu His Asp Lys Val Gly Glu Pro Tyr Ser Ile Gln Ala Tyr Ala  
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 Lys Glu Gly Val Pro Ser Glu Gly Pro Glu Thr Lys Val Glu Asn Ile  
 420 425 430  
 Gly Val Lys Thr Val Thr Ile Thr Trp Lys Glu Ile Pro Lys Ser Glu  
 435 440 445  
 Arg Lys Gly Ile Ile Cys Asn Tyr Thr Ile Phe Tyr Gln Ala Glu Gly  
 450 455 460  
 Gly Lys Gly Phe Ser Lys Thr Val Asn Ser Ser Ile Leu Gln Tyr Gly  
 465 470 475 480  
 Leu Glu Ser Leu Lys Arg Lys Thr Ser Tyr Ile Val Gln Val Met Ala  
 485 490 495  
 Ser Thr Ser Ala Gly Gly Thr Asn Gly Thr Ser Ile Asn Phe Lys Thr  
 500 505 510  
 Leu Ser Phe Ser Val Phe Glu Ile Ile Leu Ile Thr Ser Leu Ile Gly  
 515 520 525  
 Gly Gly Leu Leu Ile Leu Ile Ile Leu Thr Val Ala Tyr Gly Leu Lys  
 530 535 540  
 Lys Pro Asn Lys Leu Thr His Leu Cys Trp Pro Thr Val Pro Asn Pro  
 545 550 555 560

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Ala Glu Ser Ser Ile Ala Thr Trp His Gly Asp Asp Phe Lys Asp Lys  
                                   565                                  570                                  575  
 Leu Asn Leu Lys Glu Ser Asp Asp Ser Val Asn Thr Glu Asp Arg Ile  
                                   580                                  585                                  590  
 Leu Lys Pro Cys Ser Thr Pro Ser Asp Lys Leu Val Ile Asp Lys Leu  
                                   595                                  600                                  605  
 Val Val Asn Phe Gly Asn Val Leu Gln Glu Ile Phe Thr Asp Glu Ala  
                                   610                                  615                                  620  
 Arg Thr Gly Gln Glu Asn Asn Leu Gly Gly Glu Lys Asn Gly Thr Arg  
 625                                  630                                  635                                  640  
 Ile Leu Ser Ser Cys Pro Thr Ser Ile  
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<210> 47

<211> 1947

<212> DNA

<213> Artificial Sequence

<220>

<223> Degenerate polynucleotide sequence of SEQ ID NO:46

<221> misc\_feature

<222> (1)...(1947)

<223> n = A,T,C or G

<400> 47

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acntggwsnc	cnggnaarga	racnwsntay	acncartaya	cngtnaarmg	nacntaygcn	180
tyggngara	arcaygayaa	ytgyacnacn	aaywsnwsna	cnwsngaraa	ymgngcnwsn	240
tgywsnttyt	tyytncnmg	nathacnath	ccngayaayt	ayacnathga	rgtnngargcn	300
garaayggng	ayggngtnat	haarwsncay	atgacntayt	ggmgnytnga	raayathgcn	360
aaracngarc	cncnnaarat	httymgngtn	aarccngtny	tnggnathaa	rmgnatgath	420
carathgart	ggathaarcc	ngarytnngcn	ccngtnwsnw	sngayytnaa	rtayacnytn	480
mgnttymgna	cngtnaayws	nacnwsntgg	atggargtna	ayttygcnaa	raaymgnaar	540
gayaaraayc	aracntayaa	yytnacnggn	ytncarccnt	tyacngarta	ygtnathgcn	600
ytmgntgyg	cngtnaarga	rwsnaartty	tggwsngayt	ggwsncarga	raaratgggn	660
atgacngarg	argargcncc	ntgyggnytn	garytnctggm	gngtnytnaa	rccngcngar	720
gcngayggnm	gnmgncnngt	nmgnytnytn	tggaaraarg	cnmgnggngc	nccngtnytn	780
garaaracny	tnggntayaa	yathtggtay	tayccngarw	snaayacnaa	yytnacngar	840
acnatgaaya	cnacnaayca	rcarytngar	ytncayytn	gnggngarws	nttytggtgn	900
wsnatgathw	sntayaayws	nytnngnaar	wsnccngtn	cnacnytnmg	nathccngcn	960

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athcargara arwsnttyca rtgyathgar gtnatgcarg cntgygtngc ngargaycar 1020  
 ytngtngtna artggcarws nwsngcnytn gaygtnaaya cntggatgat hgartggtty 1080  
 ccngaygtng aywsngarcc nacnacnytn wsntgggarw sngtnwsnca rgcnacnaay 1140  
 tggacnathc arcargayaa rytnaarccn ttytggtgyt ayaayathws ngntayccn 1200  
 atgytncaayg ayaargtngg ngarccntay wsnathcarg cntaygcnaa rgarggngtn 1260  
 ccnwsngarg gncngarac naargtngar aayathggng tnaaracngt nacnathacn 1320  
 tggaargara thccnaarws ngarmgnaar ggnathatht gyaaytayac nathttytay 1380  
 cargcngarg gnggnaargg nttywsnaar acngtnaayw snwsnathyt ncartayggn 1440  
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 athytnatha cnwsnytnat hggnggnggn ytnytnathy tnathathyt nacngtngcn 1620  
 tayggnytna araarccnaa yaarytnacn cayytnygyt ggccnacngt nccnaayccn 1680  
 gcngarwsnw snathgcnac ntggcayggn gaygayttya argayaaryt naayytnaar 1740  
 garwsngayg aywsngtnaa yacngargay mgnathytna arccntgyws nacnccnwsn 1800  
 gayaarytng tnathgayaa rytngtngtn aayttyggna aygtnytnca rgarathtty 1860  
 acngaygarg cnmgnacngg ncargaraay aayytnggng gngaraaraa yggnacnmgn 1920  
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<210> 48

<211> 32

<212> PRT

<213> Homo sapiens

<400> 48

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			20					25					30		

<210> 49

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Oligonucleotide primer ZC21195

<400> 49

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<211> 23

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23

<210> 52

<211> 13

<212> PRT

<213> Homo sapiens

<400> 52

Met Lys Leu Ser Pro Gln Pro Ser Cys Val Asn Leu Gly

1

5

10

<210> 53

<211> 2903

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (497)...(2482)

<400> 53

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gaatgtccgc	aaaacattag	tttactctt	gtcgccaggt	tggagtacaa	tggcacgac	180
ttggctcact	gcaacctctg	cctcccgggt	tcaagcgatt	ctcctgcctc	agcctcccga	240
gtagctggga	ttacagttaa	caataatgca	atccatttcc	cagcataagt	gggtaagtgc	300

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cactttgact	tgggctgggc	ttaaaagcac	aagaaaagct	cgcagacaat	cagagtggaa	360
acactcccac	atcttagtgt	ggataaatta	aagtccagat	tgttcttcct	gtcctgactt	420
gtgctgtggg	aggtggagtt	gcctttgatg	caaatccttt	gagccagcag	aacatctgtg	480
gaacatcccc	tgatac	atg aag ctc tct ccc	cag cct tca tgt gtt aac	ctg		532
	Met	Lys	Leu	Ser	Pro Gln Pro Ser Cys Val Asn Leu	
	1			5		10
ggg atg atg tgg acc tgg gca ctg tgg atg ctc cct tca ctc tgc aaa	580					
Gly Met Met Trp Thr Trp Ala Leu Trp Met Leu Pro Ser Leu Cys Lys						
15 20 25						
ttc agc ctg gca gct ctg cca gct aag cct gag aac att tcc tgt gtc	628					
Phe Ser Leu Ala Ala Leu Pro Ala Lys Pro Glu Asn Ile Ser Cys Val						
30 35 40						
tac tac tat agg aaa aat tta acc tgc act tgg agt cca gga aag gaa	676					
Tyr Tyr Tyr Arg Lys Asn Leu Thr Cys Thr Trp Ser Pro Gly Lys Glu						
45 50 55 60						
acc agt tat acc cag tac aca gtt aag aga act tac gct ttt gga gaa	724					
Thr Ser Tyr Thr Gln Tyr Thr Val Lys Arg Thr Tyr Ala Phe Gly Glu						
65 70 75						
aaa cat gat aat tgt aca acc aat agt tct aca agt gaa aat cgt gct	772					
Lys His Asp Asn Cys Thr Thr Asn Ser Ser Thr Ser Glu Asn Arg Ala						
80 85 90						
tcg tgc tct ttt ttc ctt cca aga ata acg atc cca gat aat tat acc	820					
Ser Cys Ser Phe Phe Leu Pro Arg Ile Thr Ile Pro Asp Asn Tyr Thr						
95 100 105						
att gag gtg gaa gct gaa aat gga gat ggt gta att aaa tct cat atg	868					
Ile Glu Val Glu Ala Glu Asn Gly Asp Gly Val Ile Lys Ser His Met						
110 115 120						
aca tac tgg aga tta gag aac ata gcg aaa act gaa cca cct aag att	916					
Thr Tyr Trp Arg Leu Glu Asn Ile Ala Lys Thr Glu Pro Pro Lys Ile						
125 130 135 140						
ttc cgt gtg aaa cca gtt ttg ggc atc aaa cga atg att caa att gaa	964					
Phe Arg Val Lys Pro Val Leu Gly Ile Lys Arg Met Ile Gln Ile Glu						
145 150 155						

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Ala Ile Gln Glu Lys Ser Phe Gln Cys Ile Glu Val Met Gln Ala Cys	
335 340 345	
ggt gct gag gac cag cta gtg gtg aag tgg caa agc tct gct cta gac	1588
Val Ala Glu Asp Gln Leu Val Val Lys Trp Gln Ser Ser Ala Leu Asp	
350 355 360	
gtg aac act tgg atg att gaa tgg ttt ccg gat gtg gac tca gag ccc	1636
Val Asn Thr Trp Met Ile Glu Trp Phe Pro Asp Val Asp Ser Glu Pro	
365 370 375 380	
acc acc ctt tcc tgg gaa tct gtg tct cag gcc acg aac tgg acg atc	1684
Thr Thr Leu Ser Trp Glu Ser Val Ser Gln Ala Thr Asn Trp Thr Ile	
385 390 395	
cag caa gat aaa tta aaa cct ttc tgg tgc tat aac atc tct gtg tat	1732
Gln Gln Asp Lys Leu Lys Pro Phe Trp Cys Tyr Asn Ile Ser Val Tyr	
400 405 410	
cca atg ttg cat gac aaa gtt ggc gag cca tat tcc atc cag gct tat	1780
Pro Met Leu His Asp Lys Val Gly Glu Pro Tyr Ser Ile Gln Ala Tyr	
415 420 425	
gcc aaa gaa ggc gtt cca tca gaa ggt cct gag acc aag gtg gag aac	1828
Ala Lys Glu Gly Val Pro Ser Glu Gly Pro Glu Thr Lys Val Glu Asn	
430 435 440	
att ggc gtg aag acg gtc acg atc aca tgg aaa gag att ccc aag agt	1876
Ile Gly Val Lys Thr Val Thr Ile Thr Trp Lys Glu Ile Pro Lys Ser	
445 450 455 460	
gag aga aag ggt atc atc tgc aac tac acc atc ttt tac caa gct gaa	1924
Glu Arg Lys Gly Ile Ile Cys Asn Tyr Thr Ile Phe Tyr Gln Ala Glu	
465 470 475	
ggt gga aaa gga ttc tcc aag aca gtc aat tcc agc atc ttg cag tac	1972
Gly Gly Lys Gly Phe Ser Lys Thr Val Asn Ser Ser Ile Leu Gln Tyr	
480 485 490	
ggc ctg gag tcc ctg aaa cga aag acc tct tac att gtt cag gtc atg	2020

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Gly	Leu	Glu	Ser	Leu	Lys	Arg	Lys	Thr	Ser	Tyr	Ile	Val	Gln	Val	Met	
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Ala	Ser	Thr	Ser	Ala	Gly	Gly	Thr	Asn	Gly	Thr	Ser	Ile	Asn	Phe	Lys	
	510					515					520					
aca	ttg	tca	ttc	agt	gtc	ttt	gag	att	atc	ctc	ata	act	tct	ctg	att	2116
Thr	Leu	Ser	Phe	Ser	Val	Phe	Glu	Ile	Ile	Leu	Ile	Thr	Ser	Leu	Ile	
	525				530					535					540	
ggt	gga	ggc	ctt	ctt	att	ctc	att	atc	ctg	aca	gtg	gca	tat	ggt	ctc	2164
Gly	Gly	Gly	Leu	Leu	Ile	Leu	Ile	Ile	Leu	Thr	Val	Ala	Tyr	Gly	Leu	
				545					550					555		
aaa	aaa	ccc	aac	aaa	ttg	act	cat	ctg	tgt	tgg	ccc	acc	ggt	ccc	aac	2212
Lys	Lys	Pro	Asn	Lys	Leu	Thr	His	Leu	Cys	Trp	Pro	Thr	Val	Pro	Asn	
			560					565					570			
cct	gct	gaa	agt	agt	ata	gcc	aca	tgg	cat	gga	gat	gat	ttc	aag	gat	2260
Pro	Ala	Glu	Ser	Ser	Ile	Ala	Thr	Trp	His	Gly	Asp	Asp	Phe	Lys	Asp	
		575					580					585				
aag	cta	aac	ctg	aag	gag	tct	gat	gac	tct	gtg	aac	aca	gaa	gac	agg	2308
Lys	Leu	Asn	Leu	Lys	Glu	Ser	Asp	Asp	Ser	Val	Asn	Thr	Glu	Asp	Arg	
	590					595					600					
atc	tta	aaa	cca	tgt	tcc	acc	ccc	agt	gac	aag	ttg	gtg	att	gac	aag	2356
Ile	Leu	Lys	Pro	Cys	Ser	Thr	Pro	Ser	Asp	Lys	Leu	Val	Ile	Asp	Lys	
	605				610					615					620	
ttg	gtg	gtg	aac	ttt	ggg	aat	gtt	ctg	caa	gaa	att	ttc	aca	gat	gaa	2404
Leu	Val	Val	Asn	Phe	Gly	Asn	Val	Leu	Gln	Glu	Ile	Phe	Thr	Asp	Glu	
				625					630					635		
gcc	aga	acg	ggt	cag	gaa	aac	aat	tta	gga	ggg	gaa	aag	aat	ggg	act	2452
Ala	Arg	Thr	Gly	Gln	Glu	Asn	Asn	Leu	Gly	Gly	Glu	Lys	Asn	Gly	Thr	
			640					645					650			
aga	att	ctg	tct	tcc	tgc	cca	act	tca	ata	taagtgtgga	ctaaaatgcg					2502
Arg	Ile	Leu	Ser	Ser	Cys	Pro	Thr	Ser	Ile							
		655					660									

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&lt;210&gt; 54

&lt;211&gt; 662

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 54

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Ala Leu Pro Ala Lys Pro Glu Asn Ile Ser Cys Val Tyr Tyr Tyr Arg
      35          40          45
Lys Asn Leu Thr Cys Thr Trp Ser Pro Gly Lys Glu Thr Ser Tyr Thr
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Gln Tyr Thr Val Lys Arg Thr Tyr Ala Phe Gly Glu Lys His Asp Asn
65          70          75          80
Cys Thr Thr Asn Ser Ser Thr Ser Glu Asn Arg Ala Ser Cys Ser Phe
      85          90          95
Phe Leu Pro Arg Ile Thr Ile Pro Asp Asn Tyr Thr Ile Glu Val Glu
      100          105          110
Ala Glu Asn Gly Asp Gly Val Ile Lys Ser His Met Thr Tyr Trp Arg
      115          120          125
Leu Glu Asn Ile Ala Lys Thr Glu Pro Pro Lys Ile Phe Arg Val Lys
      130          135          140
Pro Val Leu Gly Ile Lys Arg Met Ile Gln Ile Glu Trp Ile Lys Pro
145          150          155          160
Glu Leu Ala Pro Val Ser Ser Asp Leu Lys Tyr Thr Leu Arg Phe Arg
      165          170          175
Thr Val Asn Ser Thr Ser Trp Met Glu Val Asn Phe Ala Lys Asn Arg
      180          185          190
Lys Asp Lys Asn Gln Thr Tyr Asn Leu Thr Gly Leu Gln Pro Phe Thr
      195          200          205
Glu Tyr Val Ile Ala Leu Arg Cys Ala Val Lys Glu Ser Lys Phe Trp
210          215          220

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Arg	Arg	Pro	Val	Arg	Leu	Leu	Trp	Lys	Lys	Ala	Arg	Gly	Ala	Pro	Val
			260					265					270		
Leu	Glu	Lys	Thr	Leu	Gly	Tyr	Asn	Ile	Trp	Tyr	Tyr	Pro	Glu	Ser	Asn
		275					280					285			
Thr	Asn	Leu	Thr	Glu	Thr	Met	Asn	Thr	Thr	Asn	Gln	Gln	Leu	Glu	Leu
	290					295					300				
His	Leu	Gly	Gly	Glu	Ser	Phe	Trp	Val	Ser	Met	Ile	Ser	Tyr	Asn	Ser
305					310					315					320
Leu	Gly	Lys	Ser	Pro	Val	Ala	Thr	Leu	Arg	Ile	Pro	Ala	Ile	Gln	Glu
				325					330					335	
Lys	Ser	Phe	Gln	Cys	Ile	Glu	Val	Met	Gln	Ala	Cys	Val	Ala	Glu	Asp
			340					345					350		
Gln	Leu	Val	Val	Lys	Trp	Gln	Ser	Ser	Ala	Leu	Asp	Val	Asn	Thr	Trp
		355					360					365			
Met	Ile	Glu	Trp	Phe	Pro	Asp	Val	Asp	Ser	Glu	Pro	Thr	Thr	Leu	Ser
	370					375					380				
Trp	Glu	Ser	Val	Ser	Gln	Ala	Thr	Asn	Trp	Thr	Ile	Gln	Gln	Asp	Lys
385					390					395					400
Leu	Lys	Pro	Phe	Trp	Cys	Tyr	Asn	Ile	Ser	Val	Tyr	Pro	Met	Leu	His
				405					410					415	
Asp	Lys	Val	Gly	Glu	Pro	Tyr	Ser	Ile	Gln	Ala	Tyr	Ala	Lys	Glu	Gly
			420				425					430			
Val	Pro	Ser	Glu	Gly	Pro	Glu	Thr	Lys	Val	Glu	Asn	Ile	Gly	Val	Lys
		435					440					445			
Thr	Val	Thr	Ile	Thr	Trp	Lys	Glu	Ile	Pro	Lys	Ser	Glu	Arg	Lys	Gly
	450					455					460				
Ile	Ile	Cys	Asn	Tyr	Thr	Ile	Phe	Tyr	Gln	Ala	Glu	Gly	Gly	Lys	Gly
465					470					475					480
Phe	Ser	Lys	Thr	Val	Asn	Ser	Ser	Ile	Leu	Gln	Tyr	Gly	Leu	Glu	Ser
				485					490					495	
Leu	Lys	Arg	Lys	Thr	Ser	Tyr	Ile	Val	Gln	Val	Met	Ala	Ser	Thr	Ser
			500					505					510		
Ala	Gly	Gly	Thr	Asn	Gly	Thr	Ser	Ile	Asn	Phe	Lys	Thr	Leu	Ser	Phe
		515					520					525			
Ser	Val	Phe	Glu	Ile	Ile	Leu	Ile	Thr	Ser	Leu	Ile	Gly	Gly	Gly	Leu
	530					535					540				
Leu	Ile	Leu	Ile	Ile	Leu	Thr	Val	Ala	Tyr	Gly	Leu	Lys	Lys	Pro	Asn
545					550					555					560

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Lys Leu Thr His Leu Cys Trp Pro Thr Val Pro Asn Pro Ala Glu Ser  
                     565                    570                    575  
 Ser Ile Ala Thr Trp His Gly Asp Asp Phe Lys Asp Lys Leu Asn Leu  
                     580                    585                    590  
 Lys Glu Ser Asp Asp Ser Val Asn Thr Glu Asp Arg Ile Leu Lys Pro  
                     595                    600                    605  
 Cys Ser Thr Pro Ser Asp Lys Leu Val Ile Asp Lys Leu Val Val Asn  
                     610                    615                    620  
 Phe Gly Asn Val Leu Gln Glu Ile Phe Thr Asp Glu Ala Arg Thr Gly  
 625                    630                    635                    640  
 Gln Glu Asn Asn Leu Gly Gly Glu Lys Asn Gly Thr Arg Ile Leu Ser  
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 Ser Cys Pro Thr Ser Ile  
                     660

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 <211> 1986  
 <212> DNA  
 <213> Artificial Sequence

<220>  
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<221> misc\_feature  
 <222> (1)...(1986)  
 <223> n = A,T,C or G

<400> 55

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athwsntgyg	tntaytayta	ymgnaaraay	ytnacntgya	cntggwsncc	nggnaargar	180
acnwsntaya	cncartayac	ngtnaarmgn	acntaygcnt	tyggngaraa	rcaygayaay	240
tgyacnacna	aywsnwnac	nwsngaraay	mgngcnwsnt	gywsnttytt	yytnccnmgn	300
athacnathc	cngayaayta	yacnathgar	gtngargcng	araayggnga	yggngtnath	360
aarwsncaya	tgacntaytg	gmgnytngar	aayathgcna	aracngarcc	nccnaarath	420
ttymgngtna	arccngtnyt	nggnathaar	mgntatgathc	arathgartg	gathaarccn	480
garytngcnc	cngtnwsnws	ngayytnaar	tayacnytnm	gnntymgnac	ngtnaaywsn	540
acnwsntgga	tggarctnaa	ytytgcnar	aaymgnaarg	ayaaraayca	racntayaay	600
ytnacnggny	tnccarccntt	yacngartay	gtnathgcny	tnmgntgygc	ngtnaargar	660
wsnaarttyt	ggwsngaytg	gwsncargar	aatatgggna	tgacngarga	rgargcnccn	720
tgyggnytn	arytntggmg	ngtnytnaar	ccngcngarg	cngayggnmg	nmgnccngtn	780
mgnytnytnt	ggaaraargc	nmgnggngcn	ccngtnytng	araaracnyt	nggntayaay	840

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Val	Gln	Pro	Leu	Gly	Val	Asn	Ala	Gly	Ile	Met	Trp	Thr	Leu	Ala	Leu		
		20					25					30					
tgg	gca	ttc	tct	ttc	ctc	tgc	aaa	ttc	agc	ctg	gca	gtc	ctg	ccg	act	383	
Trp	Ala	Phe	Ser	Phe	Leu	Cys	Lys	Phe	Ser	Leu	Ala	Val	Leu	Pro	Thr		
	35					40				45							
aag	cca	gag	aac	att	tcc	tgc	gtc	ttt	tac	ttc	gac	aga	aat	ctg	act	431	
Lys	Pro	Glu	Asn	Ile	Ser	Cys	Val	Phe	Tyr	Phe	Asp	Arg	Asn	Leu	Thr		
	50				55				60					65			
tgc	act	tgg	aga	cca	gag	aag	gaa	acc	aat	gat	acc	agc	tac	att	gtg	479	
Cys	Thr	Trp	Arg	Pro	Glu	Lys	Glu	Thr	Asn	Asp	Thr	Ser	Tyr	Ile	Val		
				70					75					80			
act	ttg	act	tac	tcc	tat	gga	aaa	agc	aat	tat	agt	gac	aat	gct	aca	527	
Thr	Leu	Thr	Tyr	Ser	Tyr	Gly	Lys	Ser	Asn	Tyr	Ser	Asp	Asn	Ala	Thr		
			85					90					95				
gag	gct	tca	tat	tct	ttt	ccc	cgt	tcc	tgt	gca	atg	ccc	cca	gac	atc	575	
Glu	Ala	Ser	Tyr	Ser	Phe	Pro	Arg	Ser	Cys	Ala	Met	Pro	Pro	Asp	Ile		
		100					105					110					
tgc	agt	gtt	gaa	gta	caa	gct	caa	aat	gga	gat	ggc	aaa	gtt	aaa	tct	623	
Cys	Ser	Val	Glu	Val	Gln	Ala	Gln	Asn	Gly	Asp	Gly	Lys	Val	Lys	Ser		
	115				120				125								
gac	atc	aca	tat	tgg	cat	tta	atc	tcc	ata	gca	aaa	acc	gaa	cca	cct	671	
Asp	Ile	Thr	Tyr	Trp	His	Leu	Ile	Ser	Ile	Ala	Lys	Thr	Glu	Pro	Pro		
	130				135				140						145		
ata	att	tta	agt	gtg	aat	cca	att	tgt	aat	aga	atg	ttc	cag	ata	caa	719	
Ile	Ile	Leu	Ser	Val	Asn	Pro	Ile	Cys	Asn	Arg	Met	Phe	Gln	Ile	Gln		
				150				155					160				
tgg	aaa	ccg	cgt	gaa	aag	act	cgt	ggg	ttt	cct	tta	gta	tgc	atg	ctt	767	
Trp	Lys	Pro	Arg	Glu	Lys	Thr	Arg	Gly	Phe	Pro	Leu	Val	Cys	Met	Leu		
		165					170					175					
cgg	ttc	aga	act	gtc	aac	agt	agc	cgc	tgg	acg	gaa	gtc	aat	ttt	gaa	815	
Arg	Phe	Arg	Thr	Val	Asn	Ser	Ser	Arg	Trp	Thr	Glu	Val	Asn	Phe	Glu		
		180				185					190						





gtg gag tgg ctc cca gaa gct gcc atg tgc aag ttc cct gcc ctt tcc	1391
Val Glu Trp Leu Pro Glu Ala Ala Met Ser Lys Phe Pro Ala Leu Ser	
370 375 380 385	
tgg gaa tct gtg tct cag gtc acg aac tgg acc atc gag caa gat aaa	1439
Trp Glu Ser Val Ser Gln Val Thr Asn Trp Thr Ile Glu Gln Asp Lys	
390 395 400	
cta aaa cct ttc aca tgc tat aat ata tca gtg tat cca gtg ttg gga	1487
Leu Lys Pro Phe Thr Cys Tyr Asn Ile Ser Val Tyr Pro Val Leu Gly	
405 410 415	
cac cga gtt gga gag ccg tat tca atc caa gct tat gcc aaa gaa gga	1535
His Arg Val Gly Glu Pro Tyr Ser Ile Gln Ala Tyr Ala Lys Glu Gly	
420 425 430	
act cca tta aaa ggt cct gag acc agg gtg gag aac atc ggt ctg agg	1583
Thr Pro Leu Lys Gly Pro Glu Thr Arg Val Glu Asn Ile Gly Leu Arg	
435 440 445	
aca gcc acg atc aca tgg aag gag att cct aag agt gct agg aat gga	1631
Thr Ala Thr Ile Thr Trp Lys Glu Ile Pro Lys Ser Ala Arg Asn Gly	
450 455 460 465	
ttt atc aac aat tac act gta ttt tac caa gct gaa ggt gga aaa gaa	1679
Phe Ile Asn Asn Tyr Thr Val Phe Tyr Gln Ala Glu Gly Gly Lys Glu	
470 475 480	
ctc tcc aag act gtt aac tct cat gcc ctg cag tgt gac ctg gag tct	1727
Leu Ser Lys Thr Val Asn Ser His Ala Leu Gln Cys Asp Leu Glu Ser	
485 490 495	
ctg aca cga agg acc tct tat act gtt tgg gtc atg gcc agc acc aga	1775
Leu Thr Arg Arg Thr Ser Tyr Thr Val Trp Val Met Ala Ser Thr Arg	
500 505 510	
gct gga ggt acc aac ggg gtg aga ata aac ttc aag aca ttg tca atc	1823
Ala Gly Gly Thr Asn Gly Val Arg Ile Asn Phe Lys Thr Leu Ser Ile	
515 520 525	
agt gtg ttt gaa att gtc ctt cta aca tct cta gtt gga gga ggc ctt	1871

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Ser Val Phe Glu Ile Val Leu Leu Thr Ser Leu Val Gly Gly Gly Leu  
 530 535 540 545

ctt cta ctt agc atc aaa aca gtg act ttt ggc ctc aga aag cca aac 1919  
 Leu Leu Leu Ser Ile Lys Thr Val Thr Phe Gly Leu Arg Lys Pro Asn  
 550 555 560

cgg ttg act ccc ctg tgt tgt cct gat gtt ccc aac cct gct gaa agt 1967  
 Arg Leu Thr Pro Leu Cys Cys Pro Asp Val Pro Asn Pro Ala Glu Ser  
 565 570 575

agt tta gcc aca tgg ctc gga gat ggt ttc aag aag tca aat atg aag 2015  
 Ser Leu Ala Thr Trp Leu Gly Asp Gly Phe Lys Lys Ser Asn Met Lys  
 580 585 590

gag act gga aac tct ggg aac aca gaa gac gtg gtc cta aaa cca tgt 2063  
 Glu Thr Gly Asn Ser Gly Asn Thr Glu Asp Val Val Leu Lys Pro Cys  
 595 600 605

ccc gtc ccc gcg gat ctc att gac aag ctg gta gtg aac ttt gag aat 2111  
 Pro Val Pro Ala Asp Leu Ile Asp Lys Leu Val Val Asn Phe Glu Asn  
 610 615 620 625

ttt ctg gaa gta gtt ttg aca gag gaa gct gga aag ggt cag gcg agc 2159  
 Phe Leu Glu Val Val Leu Thr Glu Glu Ala Gly Lys Gly Gln Ala Ser  
 630 635 640

att ttg gga gga gaa gcg aat gag tat atc tta tcc cag gaa cca agc 2207  
 Ile Leu Gly Gly Glu Ala Asn Glu Tyr Ile Leu Ser Gln Glu Pro Ser  
 645 650 655

tgt cct ggc cat tgc tgaagctacc ctgagggtcc aggacagctg tcttggtggc 2262  
 Cys Pro Gly His Cys  
 660

acttgactct ggcaggaacc tgatctctac ttttcttctc cctgtctccg gacactttct 2322  
 ctcttcatg cagagaccag gactagagcg gattctctcat ggtttgccag gctcctcagt 2382  
 ccttgctcgg gctcaggatc ttcaacaatg ccctttcttg gacactccat catccactta 2442  
 tatttatttt ttgcaacatt gtggattgaa cccagggact tgtttatgcg cgcaacttca 2502  
 gtaactgtgg cagagactta ggaatggaga tctgaccctt tgcagaaggt ttctggacat 2562  
 ccgtccctgt gtgagcctca gacagcattg tctttacttt gaatcagctt ccaagttaat 2622  
 aaaagaaaaa cagagagggt gcataacagc tcctgcttcc tgacctgctt gagttccagt 2682

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tctgacttcc tttggtgatg aacagcaatg tgggaagtgt aagctgaata aaccctttcc 2742  
tcccca 2748

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<400> 57

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Leu	Trp	Ala	Phe	Ser	Phe	Leu	Cys	Lys	Phe	Ser	Leu	Ala	Val	Leu	Pro	35	40	45	
Thr	Lys	Pro	Glu	Asn	Ile	Ser	Cys	Val	Phe	Tyr	Phe	Asp	Arg	Asn	Leu	50	55	60	
Thr	Cys	Thr	Trp	Arg	Pro	Glu	Lys	Glu	Thr	Asn	Asp	Thr	Ser	Tyr	Ile	65	70	75	80
Val	Thr	Leu	Thr	Tyr	Ser	Tyr	Gly	Lys	Ser	Asn	Tyr	Ser	Asp	Asn	Ala	85	90	95	
Thr	Glu	Ala	Ser	Tyr	Ser	Phe	Pro	Arg	Ser	Cys	Ala	Met	Pro	Pro	Asp	100	105	110	
Ile	Cys	Ser	Val	Glu	Val	Gln	Ala	Gln	Asn	Gly	Asp	Gly	Lys	Val	Lys	115	120	125	
Ser	Asp	Ile	Thr	Tyr	Trp	His	Leu	Ile	Ser	Ile	Ala	Lys	Thr	Glu	Pro	130	135	140	
Pro	Ile	Ile	Leu	Ser	Val	Asn	Pro	Ile	Cys	Asn	Arg	Met	Phe	Gln	Ile	145	150	155	160
Gln	Trp	Lys	Pro	Arg	Glu	Lys	Thr	Arg	Gly	Phe	Pro	Leu	Val	Cys	Met	165	170	175	
Leu	Arg	Phe	Arg	Thr	Val	Asn	Ser	Ser	Arg	Trp	Thr	Glu	Val	Asn	Phe	180	185	190	
Glu	Asn	Cys	Lys	Gln	Val	Cys	Asn	Leu	Thr	Gly	Leu	Gln	Ala	Phe	Thr	195	200	205	
Glu	Tyr	Val	Leu	Ala	Leu	Arg	Phe	Arg	Phe	Asn	Asp	Ser	Arg	Tyr	Trp	210	215	220	
Ser	Lys	Trp	Ser	Lys	Glu	Glu	Thr	Arg	Val	Thr	Met	Glu	Glu	Val	Pro	225	230	235	240
His	Val	Leu	Asp	Leu	Trp	Arg	Ile	Leu	Glu	Pro	Ala	Asp	Met	Asn	Gly	245	250	255	
Asp	Arg	Lys	Val	Arg	Leu	Leu	Trp	Lys	Lys	Ala	Arg	Gly	Ala	Pro	Val	260	265	270	

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Cys Pro Val Pro Ala Asp Leu Ile Asp Lys Leu Val Val Asn Phe Glu  
 610 615 620  
 Asn Phe Leu Glu Val Val Leu Thr Glu Glu Ala Gly Lys Gly Gln Ala  
 625 630 635 640  
 Ser Ile Leu Gly Gly Glu Ala Asn Glu Tyr Ile Leu Ser Gln Glu Pro  
 645 650 655  
 Ser Cys Pro Gly His Cys  
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<210> 59  
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<210> 61  
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<210> 62  
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<220>  
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<400> 62  
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<210> 63  
 <211> 23  
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<220>  
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<400> 63  
 ccagaacttt gactccttga ccg 23

<210> 64  
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 gaagtcaact tcgctaagaa ccg 23

<210> 65  
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<400> 65  
 ccgctcgagt tatattgaag ttgggcagga agac 34

<210> 66  
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 <212> DNA  
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<220>  
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<400> 66  
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<210> 67  
 <211> 33  
 <212> DNA  
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<220>  
 <223> Oligonucleotide primer ZC29124

<400> 67  
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<210> 68  
 <211> 2295  
 <212> DNA  
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<220>  
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<221> CDS



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Met	Lys	Leu	Ser	Pro	Gln	Pro	Ser	Cys	Val	Asn	Leu	Gly	Met	Met	Trp	
1				5					10						15	

acc	tgg	gca	ctg	tgg	atg	ctc	cct	tca	ctc	tgc	aaa	ttc	agc	ctg	gca	96
Thr	Trp	Ala	Leu	Trp	Met	Leu	Pro	Ser	Leu	Cys	Lys	Phe	Ser	Leu	Ala	
			20					25					30			

gct	ctg	cca	gct	aag	cct	gag	aac	att	tcc	tgt	gtc	tac	tac	tat	agg	144
Ala	Leu	Pro	Ala	Lys	Pro	Glu	Asn	Ile	Ser	Cys	Val	Tyr	Tyr	Tyr	Arg	
		35					40					45				

aaa	aat	tta	acc	tgc	act	tgg	agt	cca	gga	aag	gaa	acc	agt	tat	acc	192
Lys	Asn	Leu	Thr	Cys	Thr	Trp	Ser	Pro	Gly	Lys	Glu	Thr	Ser	Tyr	Thr	
	50					55					60					

cag	tac	aca	gtt	aag	aga	act	tac	gct	ttt	gga	gaa	aaa	cat	gat	aat	240
Gln	Tyr	Thr	Val	Lys	Arg	Thr	Tyr	Ala	Phe	Gly	Glu	Lys	His	Asp	Asn	
65					70				75						80	

tgt	aca	acc	aat	agt	tct	aca	agt	gaa	aat	cgt	gct	tcg	tgc	tct	ttt	288
Cys	Thr	Thr	Asn	Ser	Ser	Thr	Ser	Glu	Asn	Arg	Ala	Ser	Cys	Ser	Phe	
			85						90					95		

ttc	ctt	cca	aga	ata	acg	atc	cca	gat	aat	tat	acc	att	gag	gtg	gaa	336
Phe	Leu	Pro	Arg	Ile	Thr	Ile	Pro	Asp	Asn	Tyr	Thr	Ile	Glu	Val	Glu	
			100					105					110			

gct	gaa	aat	gga	gat	ggt	gta	att	aaa	tct	cat	atg	aca	tac	tgg	aga	384
Ala	Glu	Asn	Gly	Asp	Gly	Val	Ile	Lys	Ser	His	Met	Thr	Tyr	Trp	Arg	
		115				120						125				

tta	gag	aac	ata	gcg	aaa	act	gaa	cca	cct	aag	att	ttc	cgt	gtg	aaa	432
Leu	Glu	Asn	Ile	Ala	Lys	Thr	Glu	Pro	Pro	Lys	Ile	Phe	Arg	Val	Lys	
	130					135					140					

cca	gtt	ttg	ggc	atc	aaa	cga	atg	att	caa	att	gaa	tgg	ata	aag	cct	480
Pro	Val	Leu	Gly	Ile	Lys	Arg	Met	Ile	Gln	Ile	Glu	Trp	Ile	Lys	Pro	
145					150				155						160	

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gag ttg gcg cct gtt tca tct gat tta aaa tac aca ctt cga ttc agg	528
Glu Leu Ala Pro Val Ser Ser Asp Leu Lys Tyr Thr Leu Arg Phe Arg	
165 170 175	
aca gtc aac agt acc agc tgg atg gaa gtc aac ttc gct aag aac cgt	576
Thr Val Asn Ser Thr Ser Trp Met Glu Val Asn Phe Ala Lys Asn Arg	
180 185 190	
aag gat aaa aac caa acg tac aac ctc acg ggg ctg cag cct ttt aca	624
Lys Asp Lys Asn Gln Thr Tyr Asn Leu Thr Gly Leu Gln Pro Phe Thr	
195 200 205	
gaa tat gtc ata gct ctg cga tgt gcg gtc aag gag tca aag ttc tgg	672
Glu Tyr Val Ile Ala Leu Arg Cys Ala Val Lys Glu Ser Lys Phe Trp	
210 215 220	
agt gac tgg agc caa gaa aaa atg gga atg act gag gaa gaa gct cca	720
Ser Asp Trp Ser Gln Glu Lys Met Gly Met Thr Glu Glu Glu Ala Pro	
225 230 235 240	
tgt ggc ctg gaa ctg tgg aga gtc ctg aaa cca gct gag gcg gat gga	768
Cys Gly Leu Glu Leu Trp Arg Val Leu Lys Pro Ala Glu Ala Asp Gly	
245 250 255	
aga agg cca gtg cgg ttg tta tgg aag aag gca aga gga gcc cca gtc	816
Arg Arg Pro Val Arg Leu Leu Trp Lys Lys Ala Arg Gly Ala Pro Val	
260 265 270	
cta gag aaa aca ctt ggc tac aac ata tgg tac tat cca gaa agc aac	864
Leu Glu Lys Thr Leu Gly Tyr Asn Ile Trp Tyr Tyr Pro Glu Ser Asn	
275 280 285	
act aac ctc aca gaa aca atg aac act act aac cag cag ctt gaa ctg	912
Thr Asn Leu Thr Glu Thr Met Asn Thr Thr Asn Gln Gln Leu Glu Leu	
290 295 300	
cat ctg gga ggc gag agc ttt tgg gtg tct atg att tct tat aat tct	960
His Leu Gly Gly Glu Ser Phe Trp Val Ser Met Ile Ser Tyr Asn Ser	
305 310 315 320	
ctt ggg aag tct cca gtg gcc acc ctg agg att cca gct att caa gaa	1008
Leu Gly Lys Ser Pro Val Ala Thr Leu Arg Ile Pro Ala Ile Gln Glu	
325 330 335	

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aaa tca ttt cag tgc att gag gtc atg cag gcc tgc gtt gct gag gac	1056
Lys Ser Phe Gln Cys Ile Glu Val Met Gln Ala Cys Val Ala Glu Asp	
340 345 350	
cag cta gtg gtg aag tgg caa agc tct gct cta gac gtg aac act tgg	1104
Gln Leu Val Val Lys Trp Gln Ser Ser Ala Leu Asp Val Asn Thr Trp	
355 360 365	
atg att gaa tgg ttt ccg gat gtg gac tca gag ccc acc acc ctt tcc	1152
Met Ile Glu Trp Phe Pro Asp Val Asp Ser Glu Pro Thr Thr Leu Ser	
370 375 380	
tgg gaa tct gtg tct cag gcc acg aac tgg acg atc cag caa gat aaa	1200
Trp Glu Ser Val Ser Gln Ala Thr Asn Trp Thr Ile Gln Gln Asp Lys	
385 390 395 400	
tta aaa ccc ttc tgg tgc tat aac atc tct gtg tat cca atg ttg cat	1248
Leu Lys Pro Phe Trp Cys Tyr Asn Ile Ser Val Tyr Pro Met Leu His	
405 410 415	
gac aaa gtt ggc gag cca tat tcc atc cag gct tat gcc aaa gaa ggc	1296
Asp Lys Val Gly Glu Pro Tyr Ser Ile Gln Ala Tyr Ala Lys Glu Gly	
420 425 430	
gtt cca tca gaa ggt cct gag acc aag gtg gag aac att ggc gtg aag	1344
Val Pro Ser Glu Gly Pro Glu Thr Lys Val Glu Asn Ile Gly Val Lys	
435 440 445	
acg gtc acg atc aca tgg aaa gag att ccc aag agt gag aga aag ggt	1392
Thr Val Thr Ile Thr Trp Lys Glu Ile Pro Lys Ser Glu Arg Lys Gly	
450 455 460	
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Ile Ile Cys Asn Tyr Thr Ile Phe Tyr Gln Ala Glu Gly Gly Lys Gly	
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Phe Ser Lys Thr Val Asn Ser Ser Ile Leu Gln Tyr Gly Leu Glu Ser	
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Ala	Gly	Gly	Thr	Asn	Gly	Thr	Ser	Ile	Asn	Phe	Lys	Thr	Leu	Ser	Phe		
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Ser	Val	Phe	Glu	Glu	Pro	Arg	Ser	Ser	Asp	Lys	Thr	His	Thr	Cys	Pro		
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Pro	Cys	Pro	Ala	Pro	Glu	Ala	Glu	Gly	Ala	Pro	Ser	Val	Phe	Leu	Phe		
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ccc	cca	aaa	ccc	aag	gac	acc	ctc	atg	atc	tcc	cgg	acc	cct	gag	gtc		1728
Pro	Pro	Lys	Pro	Lys	Asp	Thr	Leu	Met	Ile	Ser	Arg	Thr	Pro	Glu	Val		
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Thr	Cys	Val	Val	Val	Asp	Val	Ser	His	Glu	Asp	Pro	Glu	Val	Lys	Phe		
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Asn	Trp	Tyr	Val	Asp	Gly	Val	Glu	Val	His	Asn	Ala	Lys	Thr	Lys	Pro		
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Arg	Glu	Glu	Gln	Tyr	Asn	Ser	Thr	Tyr	Arg	Val	Val	Ser	Val	Leu	Thr		
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Val	Leu	His	Gln	Asp	Trp	Leu	Asn	Gly	Lys	Glu	Tyr	Lys	Cys	Lys	Val		
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tcc	aac	aaa	gcc	ctc	cca	tcc	tcc	atc	gag	aaa	acc	atc	tcc	aaa	gcc		1968
Ser	Asn	Lys	Ala	Leu	Pro	Ser	Ser	Ile	Glu	Lys	Thr	Ile	Ser	Lys	Ala		
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aaa	ggg	cag	ccc	cga	gaa	cca	cag	gtg	tac	acc	ctg	ccc	cca	tcc	cgg		2016
Lys	Gly	Gln	Pro	Arg	Glu	Pro	Gln	Val	Tyr	Thr	Leu	Pro	Pro	Ser	Arg		
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gat gag ctg acc aag aac cag gtc agc ctg acc tgc ctg gtc aaa ggc 2064  
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 Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro  
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gag aac aac tac aag acc acg cct ccc gtg ctg gac tcc gac ggc tcc 2160  
 Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser  
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ggg aac gtc ttc tca tgc tcc gtg atg cat gag gct ctg cac aac cac 2256  
 Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His  
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 Thr Trp Ala Leu Trp Met Leu Pro Ser Leu Cys Lys Phe Ser Leu Ala  
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 Ala Leu Pro Ala Lys Pro Glu Asn Ile Ser Cys Val Tyr Tyr Tyr Arg  
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 Lys Asn Leu Thr Cys Thr Trp Ser Pro Gly Lys Glu Thr Ser Tyr Thr  
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 100 105 110  
 Ala Glu Asn Gly Asp Gly Val Ile Lys Ser His Met Thr Tyr Trp Arg  
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 Pro Val Leu Gly Ile Lys Arg Met Ile Gln Ile Glu Trp Ile Lys Pro  
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 Thr Val Asn Ser Thr Ser Trp Met Glu Val Asn Phe Ala Lys Asn Arg  
 180 185 190  
 Lys Asp Lys Asn Gln Thr Tyr Asn Leu Thr Gly Leu Gln Pro Phe Thr  
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 Glu Tyr Val Ile Ala Leu Arg Cys Ala Val Lys Glu Ser Lys Phe Trp  
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 Ser Asp Trp Ser Gln Glu Lys Met Gly Met Thr Glu Glu Glu Ala Pro  
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 His Leu Gly Gly Glu Ser Phe Trp Val Ser Met Ile Ser Tyr Asn Ser  
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 Lys Ser Phe Gln Cys Ile Glu Val Met Gln Ala Cys Val Ala Glu Asp  
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 Gln Leu Val Val Lys Trp Gln Ser Ser Ala Leu Asp Val Asn Thr Trp  
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 Phe Ser Lys Thr Val Asn Ser Ser Ile Leu Gln Tyr Gly Leu Glu Ser  
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 Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val  
 565 570 575  
 Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe  
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 Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr  
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 Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg  
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 Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly  
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 Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro  
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 Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser  
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 Met  
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 Val Gln Pro Leu Gly Val Asn Ala Gly Ile Met Trp Thr Leu Ala Leu  
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 Trp Ala Phe Ser Phe Leu Cys Lys Phe Ser Leu Ala Val Leu Pro Thr  
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 Cys Thr Trp Arg Pro Glu Lys Glu Thr Asn Asp Thr Ser Tyr Ile Val  
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 Thr Leu Thr Tyr Ser Tyr Gly Lys Ser Asn Tyr Ser Asp Asn Ala Thr  
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gag gct tca tat tct ttt ccc cgt tcc tgt gca atg ccc cca gac atc 575  
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 100 105 110

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Glu	Lys	Thr	Phe	Gly	Tyr	His	Ile	Gln	Tyr	Phe	Ala	Glu	Asn	Ser	Thr		
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Val Glu Trp Leu Pro Glu Ala Ala Met Ser Lys Phe Pro Ala Leu Ser	
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Thr Ala Thr Ile Thr Trp Lys Glu Ile Pro Lys Ser Ala Arg Asn Gly	
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 ataaaaatca tgttacagct a 2728

&lt;210&gt; 93

&lt;211&gt; 547

&lt;212&gt; PRT

&lt;213&gt; Mus musculus

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Lys Thr Phe Gln Tyr Ile Lys Ser Met Gln Ala Tyr Ile Ala Glu Pro  
 340 345 350  
 Leu Leu Val Val Asn Trp Gln Ser Ser Ile Pro Ala Val Asp Thr Trp  
 355 360 365  
 Ile Val Glu Trp Leu Pro Glu Ala Ala Met Ser Lys Phe Pro Ala Leu  
 370 375 380  
 Ser Trp Glu Ser Val Ser Gln Val Thr Asn Trp Thr Ile Glu Gln Asp  
 385 390 395 400  
 Lys Leu Lys Pro Phe Thr Cys Tyr Asn Ile Ser Val Tyr Pro Val Leu  
 405 410 415  
 Gly His Arg Val Gly Glu Pro Tyr Ser Ile Gln Ala Tyr Ala Lys Glu  
 420 425 430  
 Gly Thr Pro Leu Lys Gly Pro Glu Thr Arg Val Glu Asn Ile Gly Leu  
 435 440 445  
 Arg Thr Ala Thr Ile Thr Trp Lys Glu Ile Pro Lys Ser Ala Arg Asn  
 450 455 460  
 Gly Phe Ile Asn Asn Tyr Thr Val Phe Tyr Gln Ala Glu Gly Gly Lys  
 465 470 475 480  
 Glu Leu Ser Lys Thr Val Asn Ser His Ala Leu Gln Cys Asp Leu Glu  
 485 490 495  
 Ser Leu Thr Arg Arg Thr Ser Tyr Thr Val Trp Val Met Ala Ser Thr  
 500 505 510  
 Arg Ala Gly Gly Thr Asn Gly Val Arg Ile Asn Phe Lys Thr Leu Ser  
 515 520 525  
 Ile Ser Glu Tyr Trp Leu Gln Ala Ser Phe Trp Ser Leu Leu Arg Val  
 530 535 540  
 Gly Asn Val  
 545

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